

T300X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COLOTTA, Francesco
MUZIO, Marta
MANTOVANI, Alberto
- (ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,
AND ANTIBODIES THERETO
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BROWDY AND NEIMARK
(B) STREET: 419 Seventh Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/476,860
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IT MI 94 A 002097
(B) FILING DATE: 13-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: YUN, Allen C.
(B) REGISTRATION NUMBER: 37,971
(C) REFERENCE/DOCKET NUMBER: COLOTTA=1A
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
(D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGACTTGTA TGAAGAAGGA GGTGG

25

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding to 60-79 of B-actin
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCGCTCGTCG TCGACAACGG

20

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (D) OTHER INFORMATION: RT-PCR backward oligonucleotide complementary to 430-449
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATAGACAAC GTACATGGCT G

21

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Sequence of sIL-1ra not in common
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 24..86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GAATTCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT
Met Glu Ile Cys Arg Gly Leu Arg Ser
1 5

50

CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G
 His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser
 10 15 20

87

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
 1 5 10 15
 Phe Leu Phe His Ser
 20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Sequence of intracellular IL-1ra
 typeI not in common

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 33..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G
 Met Ala Leu
 1

42

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Sequence of intracellular IL-1ra
typeII not in common

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 33..104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT 53
Met Ala Leu Ala Asp Leu Tyr
1 5

GAA GAA GGA GGT GGA GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA 101
Glu Glu Gly Gly Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser
10 15 20

AAG G 105
Lys

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu
1 5 10 15

Gly Glu Asp Asn Ala Asp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G
was added in the first position, for computer program
reason, in order to encode the first amino acid Glu
and further in order to avoid the creation of a stop
codon in the inner region of the sequence

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|-----|-----|
| GAG | ACG | ATC | TGC | CGA | CCC | TCT | GGG | AGA | AAA | TCC | AGC | AAG | ATG | CAA | GCC | 48 |
| Glu | Thr | Ile | Cys | Arg | Pro | Ser | Gly | Arg | Lys | Ser | Ser | Lys | Met | Gln | Ala | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| TTC | AGA | ATC | TGG | GAT | GTT | AAC | CAG | AAG | ACC | TTC | TAT | CTG | AGG | AAC | AAC | 96 |
| Phe | Arg | Ile | Trp | Asp | Val | Asn | Gln | Lys | Thr | Phe | Tyr | Leu | Arg | Asn | Asn | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| CAA | CTA | GTT | GCT | GGA | TAC | TTG | CAA | GGA | CCA | AAT | GTC | AAT | TTA | GAA | GAA | 144 |
| Gln | Leu | Val | Ala | Gly | Tyr | Leu | Gln | Gly | Pro | Asn | Val | Asn | Leu | Glu | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| AAG | ATA | GAT | GTG | GTA | CCC | ATT | GAG | CCT | CAT | GCT | CTG | TTC | TTG | GGA | ATC | 192 |
| Lys | Ile | Asp | Val | Val | Pro | Ile | Glu | Pro | His | Ala | Leu | Phe | Leu | Gly | Ile | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| CAT | GGA | GGG | AAG | ATG | TGC | CTG | TCC | TGT | GTC | AAG | TCT | GGT | GAT | GAG | ACC | 240 |
| His | Gly | Gly | Lys | Met | Cys | Leu | Ser | Cys | Val | Lys | Ser | Gly | Asp | Glu | Thr | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| AGA | CTC | CAG | CTG | GAG | GCA | GTT | AAC | ATC | ACT | GAC | CTG | AGC | GAG | AAC | AGA | 288 |
| Arg | Leu | Gln | Leu | Glu | Ala | Val | Asn | Ile | Thr | Asp | Leu | Ser | Glu | Asn | Arg | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| AAG | CAG | GAC | AAG | CGC | TTC | GCC | TTC | ATC | CGC | TCA | GAC | AGT | GGC | CCC | ACC | 336 |
| Lys | Gln | Asp | Lys | Arg | Phe | Ala | Phe | Ile | Arg | Ser | Asp | Ser | Gly | Pro | Thr | |
| | | | 100 | | | | 105 | | | | | | 110 | | | |
| ACC | AGT | TTT | GAG | TCT | GCC | GCC | TGC | CCC | GGT | TGG | TTC | CTC | TGC | ACA | GCG | 384 |
| Thr | Ser | Phe | Glu | Ser | Ala | Ala | Cys | Pro | Gly | Trp | Phe | Leu | Cys | Thr | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ATG | GAA | GCT | GAC | CAG | CCC | GTC | AGC | CTC | ACC | AAT | ATG | CCT | GAC | GAA | GGC | 432 |
| Met | Glu | Ala | Asp | Gln | Pro | Val | Ser | Leu | Thr | Asn | Met | Pro | Asp | Glu | Gly | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| GTC | ATG | GTC | ACC | AAA | TTC | TAC | TTC | CAG | GAG | GAC | GAG | TAGTAC | | | | 474 |
| Val | Met | Val | Thr | Lys | Phe | Tyr | Phe | Gln | Glu | Asp | Glu | | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Ile | Cys | Arg | Pro | Ser | Gly | Arg | Lys | Ser | Ser | Lys | Met | Gln | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Arg | Ile | Trp | Asp | Val | Asn | Gln | Lys | Thr | Phe | Tyr | Leu | Arg | Asn | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Leu | Val | Ala | Gly | Tyr | Leu | Gln | Gly | Pro | Asn | Val | Asn | Leu | Glu | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |

Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile
 50 55 60
 His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr
 65 70 75 80
 Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg
 85 90 95
 Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr
 100 105 110
 Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala
 115 120 125
 Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly
 130 135 140
 Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (D) OTHER INFORMATION: A portion of the intracellular IL-1ra typeII not in common
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Gly Glu Asp
 1 5 10 15
 Asn Ala Asp Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Intracellular IL-1ra typeII

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 34..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

| | |
|--|-----|
| CAGAAGGACC TCCTGTCCTA TGAGGCCCTC CCC ATG GCT TTA GCT GAC TTG TAT | 54 |
| Met Ala Leu Ala Asp Leu Tyr | |
| 1 5 | |
| GAA GAA GGA GGT GGA GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA | 102 |
| Glu Glu Gly Gly Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser | |
| 10 15 20 | |
| AAG GAG ACG ATC TGC CGA CCC TCT GGG AGA AAA TCC AGC AAG ATG CAA | 150 |
| Lys Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln | |
| 25 30 35 | |
| GCC TTC AGA ATC TGG GAT GTT AAC CAG AAG ACC TTC TAT CTG AGG AAC | 198 |
| Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn | |
| 40 45 50 55 | |
| AAC CAA CTA GTT GCT GGA TAC TTG CAA GGA CCA AAT GTC AAT TTA GAA | 246 |
| Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu | |
| 60 65 70 | |
| GAA AAG ATA GAT GTG GTA CCC ATT GAG CCT CAT GCT CTG TTC TTG GGA | 294 |
| Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly | |
| 75 80 85 | |
| ATC CAT GGA GGG AAG ATG TGC CTG TCC TGT GTC AAG TCT GGT GAT GAG | 342 |
| Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu | |
| 90 95 100 | |
| ACC AGA CTC CAG CTG GAG GCA GTT AAC ATC ACT GAC CTG AGC GAG AAC | 390 |
| Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn | |
| 105 110 115 | |
| AGA AAG CAG GAC AAG CGC TTC GCC TTC ATC CGC TCA GAC AGT GGC CCC | 438 |
| Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro | |
| 120 125 130 135 | |
| ACC ACC AGT TTT GAG TCT GCC GCC TGC CCC GGT TGG TTC CTC TGC ACA | 486 |
| Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr | |
| 140 145 150 | |
| GCG ATG GAA GCT GAC CAG CCC GTC AGC CTC ACC AAT ATG CCT GAC GAA | 534 |
| Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu | |
| 155 160 165 | |
| GGC GTC ATG GTC ACC AAA TTC TAC TTC CAG GAG GAC GAG TAGTAC | 579 |
| Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu | |
| 170 175 180 | |

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu
1 5 10 15
Gly Glu Asp Asn Ala Asp Ser Lys Glu Thr Ile Cys Arg Pro Ser Gly
20 25 30
Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln
35 40 45
Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln
50 55 60
Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu
65 70 75 80
Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser
85 90 95
Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn
100 105 110
Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe
115 120 125
Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys
130 135 140
Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser
145 150 155 160
Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe
165 170 175
Gln Glu Asp Glu
180

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGAGTCAG CATTGTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGACTTGTA TGAAGAAGGA GGTGG

25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Gly Glu Asp
1 5 10 15

Asn Ala Asp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CCATGGCTTT AGGTAAGCTC CTTCCACTCT 60
CATT TTTTCA CCTGAGAAAT GAGAGAGGAA AATGTCTACA ATTGGTGT TT ATCAAATGCT 120
TTCAGGCTCT GGTGAGCAAG CGTCCAGGAA AATGTCAAGC GCATGGAGCT CCAGGCCTGT 180
CTGGGGGATC TGGGCACGGG GAGGCATCCA TGGGAGACCA TGCAGGCACT CTGAGGCAGG 240
GGCTGCAAGC TAGTGCCTGC TGGGGCAGCA GGTGAACAGA GAGGTGTAAC TGCTGTGACA 300
GAAGTCATGG AGTCCTTGGA GTGTGAGGGT CATT TTTCCAC TGTGATAGA ATAGGGAAAT 360
TGGTGAAATA GCCCTGT TAA ATGAGAGAAA GAACAGTGTG AGCTCAATGA GAAATACTAA 420
TAGAATGTGG CACTGAGCCA CAAGGTCTGA GGGTTGATTG ATAAGGAAGG GTGGGGACTG 480
TGGAGAATTA AGGGCTTGGC ACAGGTCAGT TCCACCAGTT GTCACAAGAG AATGCAGGCT 540
CAGGTGGCCA GAACTTCTCG CTTTTCCAGA AGAGTCCGAT ATTCTGATTT CATTATATAT 600
AGTATTCTGA TTAAACCAGA CAATAAAGCA AGCAGATAAA ATATTTAAAG TATAAGCTGC 660
CAGTTTGCAA CCTCCGGTTA GGATTTGTGT GGGGCAAAGA AAAAACTCT CAGGATCATT 720
GGTATGTAGA CTCTAATTTT AAGTTTCTAA TTTAAATTTG GCCCTGAGG CTGGGCGTGG 780
TGGCTCACAC CTGTAATCCC AGCATT TTTGG GAGGCCAAGG TGGGTGGATC TCTTGAGGTC 840

38

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|------|
| AGTTACTCTA | TGAGATAGGA | GTTTCAGCCCA | AAAGAAACAC | CATAAGAACA | AATATAATTC | 2820 |
| TTGCTTATGT | TAACCATGCA | ATGAAGCAGA | GAGAAAAAGT | CAGTGGCCTC | TTTAGGAGGA | 2880 |
| CTGTAGTGTG | GGAAGAAATA | ACTAAACTGG | GTTTCAATCC | TGGCCTGGCC | AGGATCTGGA | 2940 |
| GCAAGTGAGT | TAATCTTTCA | AAGCCTTGAG | TAGTTTATAA | AAGAATGGCC | ACTCCATAGA | 3000 |
| CAGAGTAGCC | TGAACCTTGA | GTTCTTCTAT | AAAGTCACTA | TGAATTTATA | CTCATTTTGA | 3060 |
| AAGTGGGTGT | CAATATGTCT | GTCCACTTTG | CACAGCTGTT | ATGTGGACAA | AAGGAGATCT | 3120 |
| GTGTGAAAGT | GTAACACAGA | GCCTAAACTA | TAACAGGTAA | GCAACACAGT | TGTCCC | 3176 |